

Exhibit 2: ClustalW (Amino Acid) Alignment

CLUSTAL W 2.0 multiple sequence alignment

Sequence format is Pearson
number of seqs is: 2
Sequence 1: SEQ147 311 aa
Sequence 2: T_petrophila 312 aa

comparing
paramArg[setSeqNoRange]= off
comparing

Start of Pairwise alignments

Sequences (1:2) Aligned. Score: 95
Guide tree file created: [/ebi/extserv/clustalw-
work/interactive/2007122119/clustalw2-20071221-19204050.dnd]

CLUSTAL-Alignment file created [/ebi/extserv/clustalw-
work/interactive/2007122119/clustalw2-20071221-19204050.aln]

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SEQ148      MNDLIRKYAKDQLETLKRIIEKSEGISILINGEDLSYPREVSLELPEYVEKFPPKASDVL 60
T_petrophila MNDLIRKYAKDQLEILKRIIEKSEGISILINGEDLSYPREVSLELPEYVEKFPPKASDVL 60
*****

SEQ148      EIDPEGENIGIDDIRTIKDFLNYSPELYTRKYVIVHDCERMTQQAANAFLKALEEPPEYA 120
T_petrophila EVDPEEENIGIDEIRTIKDFLNYSPELYTRKYVIVHDCERMTQQAANAFLKTLEEPPEYA 120
*:*:*  *****:*****:*****:*****:*****

SEQ148      VIVLNTRRWHYLLPTIKSRVFRVVVNPKEFRDLVKEKIGDLWEELPLLERDFKTALEAY 180
T_petrophila VIVLNTRHWHYLLPTIKSRVFRVVVNPKEFRDLVKEKIGDFWEELPLLERDFKTAFEAY 180
*****:*****:*****:*****:*****:*****

SEQ148      KLGAEKLSGLMESLKVLETEKLLKKVLSKGLEGYLACRELLERFSKVESKEFFALFDQVT 240
T_petrophila KLGAEKLSGLMESLKVLETEKLLKKALSEGLEGYLACRELLERFSKVESKEFFALFDQLT 240
*****:*****:*****:*****:*****:*****

SEQ148      NTITGKDAFLLIQRLTRIILHENTWESVED-KSVSFLDSILRVKIANLNNKLTLMNILAI 299
T_petrophila NTITGKDSFLLIQRLTRIVLHENTWESVEDQKSVSFLDSILRVKIANLNNKLTLMNILAI 300
*****:*****:*****:*****:*****

SEQ148      HRERKRGVNAWS 311
T_petrophila HRERKRGVNAWS 312
*****
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